

GenCore version 5.1.4 p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 15, 2003, 23:25:27 ; Search time 103.105 Seconds
(Without alignments)
2525.515 Million cell updates/sec

Title: US-08-978-217-2

Perfect score: 1980
Sequence: 1 MATCHESINFSNYPFSAMYS.....YKFKKNSGKKEEVLQSRN 371

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 501302 segs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1980	100.0	1915	10	US-09-964-824A-563
3	1980	100.0	1915	10	US-09-880-107-3420
4	1980	100.0	1915	10	US-09-967-768A-192

5	1980	100.0	1917	9	US-10-025-380-1105	Sequence 1105, Ap
6	1980	100.0	1917	10	US-09-922-217-1105	Sequence 1105, Ap
7	1980	100.0	1996	10	US-09-925-301-207	Sequence 207, App
8	1127	56.9	626	9	US-10-025-380-853	Sequence 853, App
9	1127	56.9	626	10	US-09-922-217-853	Sequence 853, App
10	1127	56.9	626	10	US-09-833-263-853	Sequence 853, App
11	1011	51.1	563	9	US-10-025-380-944	Sequence 944, App
12	1011	51.1	563	10	US-09-922-217-944	Sequence 944, App
13	1011	51.1	563	10	US-09-833-263-944	Sequence 944, App
14	903	45.6	502	10	US-10-076-622-282	Sequence 282, App
15	903	45.6	502	10	US-09-604-287A-282	Sequence 282, App
16	903	45.6	502	10	US-09-339-338-282	Sequence 282, App
17	903	45.6	502	12	US-10-007-803-282	Sequence 282, App
18	822	41.5	499	10	US-09-998-598-2290	Sequence 2290, Ap
19	652	32.9	437	10	US-09-998-598-2216	Sequence 2216, Ap
20	618	31.2	355	10	US-09-867-701-4818	Sequence 4818, Ap
21	558	28.2	1429	10	US-09-764-864-330	Sequence 330, App
22	556.5	28.1	1426	10	US-09-925-297-309	Sequence 309, App
23	519.5	26.2	852	9	US-09-232-880-44	Sequence 44, Appl
24	519.5	26.2	852	9	US-10-012-896-44	Sequence 44, Appl
25	519.5	26.2	852	9	US-09-895-793-44	Sequence 44, Appl
26	519.5	26.2	852	9	US-09-895-814-44	Sequence 44, Appl
27	519.5	26.2	852	10	US-09-759-143-44	Sequence 44, Appl
28	519.5	26.2	852	10	US-09-780-663-44	Sequence 44, Appl
29	519.5	26.2	852	10	US-09-030-606-44	Sequence 44, Appl
30	519.5	26.2	852	10	US-09-822-827-44	Sequence 44, Appl
31	519.5	26.2	852	10	US-09-115-453-44	Sequence 44, Appl
32	442	22.3	5045	9	US-09-974-298-12	Sequence 12, Appl
33	435	22.0	440	10	US-09-960-352-11873	Sequence 11873, A
34	374	18.9	451	10	US-09-998-598-32	Sequence 32, Appl
35	305	15.4	174	10	US-09-998-598-1740	Sequence 1740, Ap
36	290	14.6	593	10	US-09-864-761-14745	Sequence 14745, A
37	285	14.4	196	10	US-09-864-761-31274	Sequence 31274, A
38	240	12.1	3591	9	US-10-098-841-45	Sequence 45, Appl
39	240	12.1	3663	9	US-10-098-841-44	Sequence 44, Appl
40	238.5	12.0	1894	10	US-09-126-945B-1	Sequence 1, Appl
41	238.5	12.0	1905	10	US-09-866-356-2	Sequence 2, Appl
42	234.5	11.8	1752	10	US-09-850-799-1	Sequence 1, Appl
43	233	11.8	2188	10	US-09-920-300A-1716	Sequence 1716, Ap
44	233	11.8	2188	12	US-10-033-528-1716	Sequence 1716, Ap
45	233	11.8	2268	10	US-09-920-300A-1693	Sequence 1693, Ap

ALIGNMENTS

RESULT 1
US-09-964-824A-101
; Sequence 101, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-101
Alignment Scores: 2.16e-184 Length: 1915
Pred. No.: 1980.00 Matches: 371
Score:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-08-978-217-2 (1-371) x US-09-964-824A-101 (1-1915)

QY 1 MetAlaAlaThrCysGluIleSerAsnIlePheSerAsnTyrPheSerAlaMetTyrSer 20
DB 120 ATGGCTGCAACCTGTAGATTAGCAACATTTTACCACTACTTCACTGATGATGACAGC 179
QY 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyValAspAspLeu 40
DB 180 TGGAGGAGCTCCACCTGGCTCTGTCTCCCTCCGCGCACCTTGGGGCCAGATGACTTG 239
QY 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluValAlaSerTyrLeu 60
DB 240 GTACTGACCTTACGACACCCCAAGATGATGATGAGGAGTACAGAGAGGCCCAAGCTTG 299
QY 61 GlyGluGlnProGlnPheThrPheTyrSerIleValLeuAspTyrIleSerTyrGlnVal 80
DB 300 GGGGAACACGCCCACTGCTGTGTGAAGACGCAAGCTTCTGAGCTGATGATCAAGTG 359
QY 81 GlyValAsnIleTyrAspAlaSerAlaIleAspPheSerTyrGlyAspMetLeuGlyVal 100
DB 360 GAGAAGAACAGTACACCAAGCCGCACTTGAATGATGATGATGATGATGATGATGATG 419
QY 101 ThrLeuCysAsnCysAlaLeuGluGluValAspGlyPheGlyPheLeuGlyAspGln 120
DB 420 ACCCTCTGCAATTGTGCTTGAAGGCTGCTGTGTGCTTGTGCTTGTGCTTGTGCTTGT 479
QY 121 LeuHsAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrIleIle 140
DB 480 CTCATGCGCCAGCTGAGACCTCACTTCAGCTTCTTGTAGATGATGATGATGATGATGAT 539
QY 141 GluLeuLeuGluValAspGlyMetAlaPheGlnGluValLeuAspProGlyProPheAsp 160
DB 540 GAGCTGCTGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 599
QY 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHs 180
DB 600 CAGGGAGACCCCTTTGGCCAGAGCTGCTGAGACGAGTCAAGACCCAGCCCTTACAC 659
QY 181 ProGlySerCysGlyValAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
DB 660 CCGGAGAGCTGTGGGCGACAGAGCCCTCCCTCGCAGCTGATGATGATGATGATGATG 719
QY 201 ThrGlyAlaSerTyrSerSerSerSerSerSerSerSerGlyGlySerAspValAspLeuAsp 220
DB 720 ACTGTGCTTCTTCGAGAGCTCCCACTCTCAAGCTCCGAGTGAAGTGAAGTGAAGTGA 779
QY 221 ProThrAspGlyValLeuPheProSerAspGlyPheArgAspCysValValAspPro 240
DB 780 CCCACGATGGCAAGCTTCCCAAGAGTGTTCGTGATGCGCAAGAGGGGGAGTCCC 839
QY 241 LysHsIleGlyValArgValArgGlyArgProArgLysLeuSerIleGlyTyrTyrAspCys 260
DB 840 AAGCAAGGGAACCGGAAGAGAGCGCGCCCGCAAGCTAGCAAGAGAGAGAGAGAGAGAG 899
QY 261 LeuGluGlyValValValValValValValValValValValValValValValValVal 280
DB 900 CTCGAGGCGCAAG 959
QY 281 AspIleLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 300
DB 960 GACATCTCTATCACCAGGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019
QY 301 GlyValAlaPheValPheValPheValPheValPheValPheValPheValPheValPhe 320
DB 1020 GCGCTCTTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
QY 321 AsnSerAsnMetThrTyrGluValValValValValValValValValValValValVal 340

DB 1080 AACAGCAACATGACCTTACGAGAGCTGAGCCGCGCATGAGTACTACTACAAAGCGAG 1139
QY 341 IleLeuGluArgValAlaAspGlyValArgValValTyrLysPheGlyLysAsnSerSerGly 360
DB 1140 ATCTTGGAACGGGTGGATGGCGCGGAGCTCGTCTACAAAGTGTGGCAAAAGTCAAGCGCG 1199
QY 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
DB 1200 TGGAGGAGAGAAAGAGTCTCCAGAGTGGAAAC 1232

RESULT 2

US-09-964-824A-563
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964, 824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236, 033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-563

Alignment Scores:
Pred. No.: 2,16e-184 Length: 1915
Score: 1980.00 Matches: 371
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-08-978-217-2 (1-371) x US-09-964-824A-563 (1-1915)

QY 1 MetAlaAlaThrCysGluIleSerAsnIlePheSerAsnTyrPheSerAlaMetTyrSer 20
DB 120 ATGGCTGCAACCTGTAGATTAGCAACATTTTACCACTACTTCACTGATGATGACAGC 179
QY 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyValAspAspLeu 40
DB 180 TGGAGGAGCTCCACCTGGCTCTGTCTCCCTCCGCGCACCTTGGGGCCAGATGACTTG 239
QY 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluValAlaSerTyrLeu 60
DB 240 GTACTGACCTTACGACACCCCAAGATGATGATGAGGAGTACAGAGAGGCCCAAGCTTG 299
QY 61 GlyGluGlnProGlnPheThrPheTyrSerIleValLeuAspTyrIleSerTyrGlnVal 80
DB 300 GGGGAACGCCCACTGCTGTGTGAAGACGCAAGCTTCTGAGCTGATGATGATGATGATG 359
QY 81 GlyValAsnIleTyrAspAlaSerAlaIleAspPheSerTyrGlyAspMetLeuGlyVal 100
DB 360 GAGAAGAACAGTACACCAAGCCGCACTTGAATGATGATGATGATGATGATGATGATG 419
QY 101 ThrLeuCysAsnCysAlaLeuGluGluValAspGlyPheGlyPheLeuGlyAspGln 120
DB 420 ACCCTCTGCAATTGTGCTTGAAGGCTGCTGTGTGCTTGTGCTTGTGCTTGTGCTTGT 479
QY 121 LeuHsAlaGlnLeuArgAspLeuThrSerSerSerSerSerSerSerSerGlyGlySer 140
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; APPLICANT: Carter, Derrick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.471C14
 ; CURRENT APPLICATION NUMBER: US/10/025.380
 ; CURRENT FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 1129
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1105
 ; LENGTH: 1917
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-025-380-1105

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 Qy 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40
 Db 182 TCGAGAGACTCCACCTGGCTCTGTTCCCTCTGTCACCTTGGGGCGAGATGACTTG 241
 Qy 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluValSerTyrLeu 60
 Db 242 GTACTGACCTGACCAACCCCAAGTTCATTGAGGATGACAGAAAGCCAGCTGGTTG 301
 Qy 61 GlyGluGlnProGlnPheTyrSerTyrThrGlnValLeuAspTyrPheGlnVal 80
 Db 302 GGGGACAGCCCGAGTCTGTGTCGAAAGCGAGGTTCTGATGATGATGATGATGATG 361
 Qy 81 GluLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetCaspGlyAla 100
 Db 362 GAGAGAAACAAGTACGACGCAAGCGCCCTTCACTTCACATGATGATGATGATGATG 421
 Qy 101 ThrLeuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 120
 Db 422 ACCCTGTCGAATGTGCTTGTGAGAGCTGTGCTGTGCTTGTGCTTGTGCTTGTGCT 481
 Qy 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerSerAspGluLeuSerTyrPhe 140
 Db 482 CTCATGCTCCAGCTGCGAGACTCTCACTTCCAGCTTCTTGATGAGCTCAGTTGATCAT 541
 Qy 141 GluLeuLeuGluLysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAsp 160
 Db 542 GAGCTGCTGAGAGAGATGCGATGCTTCCAGAGCGCCCTTACAGACCCCTTTTAC 601
 Qy 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
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 Qy 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
 Db 662 CCGGCGAGCTGTGCGAGAGAGCCCTTCCCTGCGAGCTTGAAGCTTCCACCGCAGG 721
 Qy 201 ThrGlyAlaSerArgSerSerHisSerSerSerSerGlyGlySerAspValAspLeuAsp 220
 Db 722 ACTGCTCTTCTCGAGAGCTCCACCTCCAGACTCCGCTGAGAGTGAAGTGAAGTGAAGT 781
 Qy 221 ProThrAspGlyLysLeuPheProSerSerAspGlyPheArgAspCysLeuLysGlyAspPro 240
 Db 782 CCCACTGATGGCAAGCTCTTCCCGACGATGATGATGATGATGATGATGATGATGATG 841
 Qy 241 LysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyLysTyrTrpAspCys 260

Db 842 AAGCAGCGAAGCGGAAAGAGAGCGGCGCCCGAAAGCTGAGCAAGAGTACTGGAGCTGT 901
 Qy 261 LeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrPheGluPheIleArg 280
 Db 902 CTGAGGCGCAAGAAAGCAAGACAGCGCCCGAGAGCCACCACTGTGTGGATCATATCCG 961
 Qy 281 AspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTyrPheGluAsnArgHisGlu 300
 Db 962 GACATCTCATCCACCGGAGCTCAACGAGGGCTTCATGAAAGTGGAGAAATCGGCATGAA 1021
 Qy 301 GlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTyrPheGlyGlnLysLys 320
 Db 1022 GCGCTTCAAGTTCCTGCGCTCGAGCTGTGCGCCCACTATGCGGCCCAAAAAAG 1081
 Qy 321 AsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlu 340
 Db 1082 AACGACAACTGACCTTACGAAAGCTAGCGCGGCTATGAGTACTTCAACAAAGGAG 1141
 Qy 341 IleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGly 360
 Db 1142 ATCTGGAAGCGGTGATGAGCGCGGCTGCTCTACAAAGTTGGCAAAACTCAAGCGGC 1201
 Qy 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
 Db 1202 TCGAAGAGAGAAAGAGTTCCTCCAGATGCGAAG 1234

RESULT 6

US-09-922-217-1105
 ; Sequence 1105, Application US/09922217
 ; Patent No. US20020076414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Smith, Carole Lynn
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.
 ; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.471C13
 ; CURRENT APPLICATION NUMBER: US/09/922.217
 ; NUMBER OF SEQ ID NOS: 1124
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1105
 ; LENGTH: 1917
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-922-217-1105

Alignment Scores:
 Prod. No.: 2.16e-184 Length: 1917
 Score: 1980.00 Matches: 371
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-08-978-217-2 (1-371) x US-09-922-217-1105 (1-1917)
 Qy 1 MetAlaAlaThrCysGluLeuSerAsnIlePheSerAsnTyrrPheSerAlaMetTySer 20
 Db 122 ATGCTGCAACCTGTGAGATTAGCAACATTTTATGCAACTACTTCACTGATGATGAC 181
 Qy 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40

Db 182 TCGAGAGACTCCACCTGGCTCTGTTCCCTGCTCCACCTTTGGGGCCGATGACTTTG 241
Qy 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluValAspTyrLeu 60
Db 242 GACTGACCTGATGACGACCCCGATGATGATGAGGATGACGAGAGCCGCTGGTTG 301
Qy 61 GlyGluGlnProGlnPheTyrSerLeuThrGlnValLeuAspTyrPheSerTyrGlnVal 80
Db 302 GGGGAACAGCCCCAGCTTGTGTGTAAGAGCAGAGGTTCTGAGCTGAGTACCAAGTG 361
Qy 81 GlyValAsnLeuTyrAspAlaSerAlaLeuAspPheSerTyrCysAspMetSerPheVal 100
Db 362 GAGAAAGAACATGATGACGACCAAGCCGATGACTTCTCAGATGATGATGATGATGATG 421
Qy 101 ThrLeuCysAsnCyAspAlaLeuGluGluLeuValPheGlyProLeuGlyAspGln 120
Db 422 ACCCTCTGCAATGTGCTTGTGAGAGAGCTGCTGTGTTGGGCTTGGGGGACCA 481
Qy 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrPheLeu 140
Db 482 CTCCATGCCCCAGCTGAGACCTCACTTCCAGCTTCTGATGAGCTCAGTTGATCATT 541
Qy 141 GluLeuLeuGluValAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
Db 542 GAGCTGTGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 601
Qy 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnAlaLeuSerProTyrHis 180
Db 602 CAGGGGACCCCTTTGGCCAGAGAGCTGTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAG 661
Qy 181 ProGlySerCysGlyValAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
Db 662 CCGGAGAGCTGTGGGAG 721
Qy 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
Db 722 ACTGTGTCTTCTGAGAGCTCCACTCTCTGAGCTCGGTGAGAGAGAGAGAGAGAGAGAG 781
Qy 221 ProThrAspGlyValLeuPheProSerAspGlyPheArgAspCysValSerGlyAspPro 240
Db 782 CCCATGATGAGAGAGCTCTTCCCGAGAGATGTTTCTGATGATGATGATGATGATGATG 841
Qy 241 LysHisGlyValArgValArgGlyArgProArgGlyValSerLeuSerLeuGlyTyrTyrAspCys 260
Db 842 AAGCAGCGGAG 901
Qy 261 LeuGluGlyValLeuSerLeuSerHisAlaProArgGlyThrHisLeuTyrPheLeuArg 280
Db 902 CTGAG 961
Qy 281 AspLeuLeuHisAspProGluLeuAsnGluGlyLeuMetLeuTyrPheGluAsnArgHisGlu 300
Db 962 GACATCTCTATCCACCGAGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
Qy 301 GlyValPheValPheLeuArgSerGlyAlaValAlaGlnLeuTyrPheGlyGlnValSerLeu 320
Db 1022 GGGCTCTTCAAGCTCTGCGGTCTCGAGAGCTGTGGCCCACTATGAGGAGAGAGAGAGAG 1081
Qy 321 AsnSerAsnMetThrTyrGluValLeuSerArgAlaMetArgTyrTyrTyrValSerGlu 340
Db 1082 AACACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1141
Qy 341 IleLeuGluArgValAspGlyArgArgLeuValTyrValPheGlyValSerAsnSerSerGly 360
Db 1142 ATCTGGAAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1201
Qy 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
Db 1202 TCGAAG 1234
RESULT 7
US-09-925-301-207
; Sequence 207, Application US/09925301

; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P1106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 207
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-207
Alignment Scores:
Pred. No.: 2,296-184 Length: 1996
Score: 1980.00 Matches: 371
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-08-978-217-2 (1-371) x US-09-925-301-207 (1-1996)
Qy 1 MetAlaAlaThrCysGluIleSerAsnIlePheSerAsnTyrPheSerAlaMetCysSer 20
Db 141 ATGGCTGCAACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 200
Qy 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyValAspAspLeu 40
Db 201 TCGAGAGACTCCACCTGAGCTGTGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 260
Qy 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluValAspTyrLeu 60
Db 261 GACTGACCTGATGACGACCCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 320
Qy 61 GlyGluGlnProGlnPheTyrSerLeuThrGlnValLeuAspTyrPheSerTyrGlnVal 80
Db 321 GGGGAACAGCCCCAGCTTGTGTGTAAGAGCAGAGGTTCTGAGCTGAGTACCAAGTG 380
Qy 81 GlyValAsnLeuTyrAspAlaSerAlaLeuAspPheSerArgCysAspMetSerPheVal 100
Db 381 GAGAAAGAACATGATGACGACCAAGCCGATGATGATGATGATGATGATGATGATGATGATG 440
Qy 101 ThrLeuCysAsnCyAspAlaLeuGluGluLeuValPheGlyProLeuGlyAspGln 120
Db 441 ACCCTCTGCAATGTGCTTGTGAGAGAGCTGCTGTGTTGGGCTCTGGGGGACCA 500
Qy 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrPheLeu 140
Db 501 CTCCATGCCCCAGCTGAGAGCTCACTTCCAGCTTCTGATGAGACTCAGTTGGATCTATT 560
Qy 141 GluLeuLeuGluValAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
Db 561 GAGCTGTGAGAAAG 620
Qy 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnAlaLeuSerProTyrHis 180
Db 621 CAGGGGACCCCTTTGGCCAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
Qy 181 ProGlySerCysGlyValAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
Db 681 CCGGAGAGCTGTGGGAG 740
Qy 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
Db 741 ACTGTGTCTTCTGAGAGCTCCACTCTCAGACTCGGTGAGAGAGAGAGAGAGAGAGAGAGAG 800

Qy 221 ProThraSpGlyLysLeuPheProSerAspGlyPheAlaArgAspCysLysGlyAspPro 240
 Db 801 CCCACTGATGGCAAGCTCTTCCCGAGCATGTTCGTGACTGCAAGAAAGGGGAGTCCC 860
 Qy 241 LysHisGlyLysAspGlyAspArgGlyArgProArgGlyLeuSerLysGlyLysTrpAspCys 260
 Db 861 AACACGCGGGAAGCGAAACGAGCGCGCCCGAAAGCTGAGCAAAAGAGTACTGGGACTGT 920
 Qy 261 LeuGluGlyLysLysSerLysHisAlaProArgGlyLysHisLeuTrpGluPheIleArg 280
 Db 921 CTCGAGGGCAAGAAAGACAGACAGCCGCCAGAGCACCCACTGTGGAGATTATCCGG 980
 Qy 281 AspIleLeuIleHisProGluLeuAsnGluLysLeuMetLysTrpGluAsnArgHisGlu 300
 Db 981 GACATCTCTCATCCACCGGAGCTCAACGAGGCTCATGAAAGTGGGAGAAATCCGGCATGAA 1040
 Qy 301 GlyValPheLysPheLeuArgSerGluAlaValAlaGluLeuTrpGluLysLysLys 320
 Db 1041 GGGCTCTTCAAGTTCCCGCGCTCCGAGCGTGTGGCCCAACTATGGGCGCAAAAAG 1100
 Qy 321 AsnSerAsnMetThrTyArgLysLeuSerArgAlaMetArgTyTrpTyTrpLysArgGlu 340
 Db 1101 AACAGCAACTGACCTTACGAGAACTGAGCCGGCCATGAGTTCTACTACAAACGGGAG 1160
 Qy 341 IleLeuGluArgValAspGlyArgArgLeuValTyTrpLysPheGlyLysAsnSerSerGly 360
 Db 1161 ATCTTGAAACGGGTGGATGGCGCGGACTGCTTACAAAGTTTGGCAAAAACCTCAAGCGGC 1220
 Qy 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
 Db 1221 TGGAAAGAGGAAGAGGTTCCTCCAGAGTCGGAAAC 1253

RESULT 8

US-10-025-380-853/c
 ; Sequence 853, Application US/10025380
 ; Publication No. US20020182191A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeline Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Smith, Carole L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick Thomas S.
 ; APPLICANT: Carter, Darick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.471C14
 ; CURRENT APPLICATION NUMBER: US/10/025,380
 ; NUMBER OF SEQ ID NOS: 1129
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 853
 ; LENGTH: 626
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-025-380-853

Alignment Scores:
 Pred. No.: 1,26e-101 Length: 626
 Score: 1127.00 Matches: 208
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 56.92% Indels: 0
 DB: 9 Gaps: 0
 LENGTH: 626

US-08-978-217-2 (1-371) x US-10-025-380-853 (1-626)
 Qy 53 GlyThrGluLysAlaSerTrpLeuGlyGluGlnProGlnPheTrpSerLysTrnGlnVal 72
 Db 624 GGTACAGAAAGGCGACCTGTTGGGGAACAGCCCAAGTTCTGTGTAAGACCGAGTT 565
 Qy 73 LeuAspTrpIleSerTyArgValGluLysAsnLysTyArgAlaSerAlaIleAspPhe 92
 Db 564 CTGAGCTGATCAAGCTCCAAAGTGAAGAAACAAGTACAGCAAGCGCATTTGACTTC 505
 Qy 93 SerArgCysAspMetLaspGlyAlaThrLeuCysAsnCysAlaLeuGluGluLeuArgLeu 112
 Db 504 TCAGAGTGTACATGATGAGCGCCACCCCTTGCAATGTGCTTGGAGAGCTGGCTGTG 445
 Qy 113 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuTrnSerSer 132
 Db 444 GTCTTGGGCTCTGGGGGACCAACTCATGCCCAGCTGGAGACCTTCCAGCTCT 385
 Qy 133 SerAspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetAlaPheGlnGlu 152
 Db 384 TCTGATAGCTCATGTTGATCATTTGAGCTCTGGAGAAAGATGGCATGGCTTCCAGAG 325
 Qy 153 AlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAsp 172
 Db 324 GCCCTAGACCAGGGCCCTTTGACCAAGGCGAGCCCTTTGCCCGAGAGCTGTGGAGAC 265
 Qy 173 GlyGlnGlnAlaSerProTyTrnHisProGlySerCysGlyAlaGlyAlaProSerProGly 192
 Db 264 GGTAGGACGACGCCCCCTTACACCCCGGAGCTGTGGCGAGAGCCCTTCCCGGCGC 205
 Qy 193 SerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerHisSerSerAspSer 212
 Db 204 AGCTCTGACGCTCTCCACCGAGGAGCTGTGCTTCTCGAGCTCCACTCTCGAGCTCC 145
 Qy 213 GlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPheProSerAspGlyPhe 232
 Db 144 GGTGGAAGTACGTCGACCTGATCCCATGATGGCAAGCTCTTCCCGAGAGTGTCTT 85
 Qy 233 ArgAspCysLysLysGlyAspProLysHisGlyLysArgLysAspGlyArgProArgLys 252
 Db 84 CGTACTGCAAGAAAGGGGAGTCCCAAGACAGGGAAGCGAAACGAGCGCGCCGAAAG 25
 Qy 253 LeuSerLysGluTyTrpAspCys 260
 Db 24 CTGAGCAAAAGAGTACTGGAGCTGT 1

RESULT 9

US-09-922-217-853/c
 ; Sequence 853, Application US/09922217
 ; Patent No. US20020076414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeline Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Smith, Carole Lynn
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.471C13
 ; CURRENT APPLICATION NUMBER: US/09/922,217
 ; NUMBER OF SEQ ID NOS: 1124
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 853
 ; LENGTH: 626

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-853

Alignment Scores:
Pred. No.: 1,266-101 Length: 626
Score: 1127.00 Matches: 208
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.92% Indels: 0
DB: 10 Gaps: 0

US-08-978-217-2 (1-371) x US-09-922-217-853 (1-626)

QY 53 GYTHRGULYALASERTYPLEUGIUGINPROGINPHETPSERYTHRGINVA 72
DB 624 GGTACAGAGAGAGCCAGCTGGTTGGGGGAACAGCCCACTTCTGTGCAAGACGCGAGTT 565
QY 73 LEUAAPTPILESERTYRGINVAIGULYSAENLYSTYRAAPLASERLAALAEAPHE 92
DB 564 CTGGACTGGATCAGCTACCAAGTGGAAGAACAAAGTACGACGCAAGCCCACTTGACTTC 505
QY 93 SERATGCVASPMETASPGIYALATHRLEUCYBANCYBALALEUGIUGILEUARGLEU 112
DB 504 TCACGATGTGACATGATGATGGCCCACTCTGTGCAATTGTGCTTGAGAGAGCTGCTTG 445
QY 113 VALPHEGIYPROLEUGIYASPGINLEUHSALAGINLEUARGASPLEUTHSERSESR 132
DB 444 GCTTTGGGCTCTGGGGGAGCCCACTCCATGCCCACTCGAGACTCTCACTTCCAGCTCT 385
QY 133 SERAEPGULEUSERTYPILEIIEGULEUENUGIULYASPGIYMETALAEHEGINLU 152
DB 384 TCTGATGACCTCAGTTGATGATGATGCTGAGAGAAAGATGGCATGGCTTCCAGGAG 325
QY 153 ALALEUASPPROGIYPROPHASPGINGIYSETPROPHALAGINLEUENUEASPA 172
DB 324 GCCCTAGACCCAGGGCCCTTTGACCCAGGSCAGCCCTTTGCCAGGAGCTGCTGACGAGC 265
QY 173 GIYGINGINALASERTYPIYTHIRHISPROGIYSESGIYALAGIYALAEPROSERPROGIY 192
DB 264 GGTCAAGAACGCCAGCCCTTTGACCCAGGAGCTGCTGAGGAGAGCCCTTCCCGGAGC 205
QY 193 SERSEASPPVALISERTYTHIRALAGIYTHIRGIYALASERTYSESRHISERSEASPPSR 212
DB 204 AGCTGTGACGTCTCCACCCAGGAGCTGCTGCTTCCGAGCTCCCACTTCCAGACTCC 145
QY 213 GIYGISERASPPVALASPLEUASPPROTHIRASPGIYLYLEUPHEROSERASPGIYPHE 232
DB 144 GGTGAAGAGTACGTGACCTGATCCCACTGATGGCAAGCTCTTCCCAAGCATGTGTTT 85
QY 233 ARGASPCYLYLYSGIYASPPROLYSHIAGIYLYSARGLYSARGIYARPPROARGLYS 252
DB 84 CGTGACTGCAGAGAGGGGATCCCAAGCAAGCGGAAAGCGAAGCCGCGCCCGAAG 25
QY 253 LEUSERTYSGIUTYRTYRASPYS 260
DB 24 CTGAGCAAAAGTACTGGGACTGT 1

RESULT 10
US-09-833-263-853/c
; Sequence 853, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stoik, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-853

Alignment Scores:
Pred. No.: 1,266-101 Length: 626
Score: 1127.00 Matches: 208
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.92% Indels: 0
DB: 10 Gaps: 0

US-08-978-217-2 (1-371) x US-09-833-263-853 (1-626)

QY 53 GYTHRGULYALASERTYPLEUGIUGINPROGINPHETPSERYTHRGINVA 72
DB 624 GGTACAGAGAGAGCCAGCTGGTTGGGGGAACAGCCCACTTCTGTGCAAGACGCGAGTT 565
QY 73 LEUAAPTPILESERTYRGINVAIGULYSAENLYSTYRAAPLASERLAALAEAPHE 92
DB 564 CTGGACTGGATCAGCTACCAAGTGGAAGAACAAAGTACGACGCAAGCCCACTTGACTTC 505
QY 93 SERATGCVASPMETASPGIYALATHRLEUCYBANCYBALALEUGIUGILEUARGLEU 112
DB 504 TCACGATGTGACATGATGATGGCCCACTCTGTGCAATTGTGCTTGAGAGAGCTGCTTG 445
QY 113 VALPHEGIYPROLEUGIYASPGINLEUHSALAGINLEUARGASPLEUTHSERSESR 132
DB 444 GCTTTGGGCTCTGGGGGAGCCCACTCCATGCCCACTCGAGACTCTCACTTCCAGCTCT 385
QY 133 SERAEPGULEUSERTYPILEIIEGULEUENUGIULYASPGIYMETALAEHEGINLU 152
DB 384 TCTGATGACCTCAGTTGATGATGATGCTGAGAGAAAGATGGCATGGCTTCCAGGAG 325
QY 153 ALALEUASPPROGIYPROPHASPGINGIYSETPROPHALAGINLEUENUEASPA 172
DB 324 GCCCTAGACCCAGGGCCCTTTGACCCAGGAGCTGCTGAGGAGAGCCCTTCCCGGAGC 265
QY 173 GIYGINGINALASERTYPIYTHIRHISPROGIYSESGIYALAGIYALAEPROSERPROGIY 192
DB 264 GGTCAAGAACGCCAGCCCTTTGACCCAGGAGCTGCTGAGGAGAGCCCTTCCCGGAGC 205
QY 193 SERSEASPPVALISERTYTHIRALAGIYTHIRGIYALASERTYSESRHISERSEASPPSR 212
DB 204 AGCTGTGACGTCTCCACCCAGGAGCTGCTGCTTCCGAGCTCCCACTTCCAGACTCC 145
QY 213 GIYGISERASPPVALASPLEUASPPROTHIRASPGIYLYLEUPHEROSERASPGIYPHE 232
DB 144 GGTGAAGAGTACGTGACCTGATCCCACTGATGGCAAGCTCTTCCCAAGCATGTGTTT 85
QY 233 ARGASPCYLYLYSGIYASPPROLYSHIAGIYLYSARGLYSARGIYARPPROARGLYS 252
DB 84 CGTGACTGCAGAGAGGGGATCCCAAGCAAGCGGAAAGCGAAGCCGCGCCCGAAG 25
QY 253 LEUSERTYSGIUTYRTYRASPYS 260
DB 24 CTGAGCAAAAGTACTGGGACTGT 1

RESULT 11
US-10-025-380-944/c
; Sequence 944, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stoik, John A.
; APPLICANT: Wang, Tongtong
```



```
APPLICANT: Jiang, Yugui
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Ranger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025.380
NUMBER OF SEQ ID NOS: 2001-12-19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 944
LENGTH: 563
TYPE: DNA
ORGANISM: Homo sapiens
US-10-025-380-944
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Alignment Scores:
Pred. No.: 2,41e-90 Length: 563
Score: 1011.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.06% Indels: 0
DB: Gaps: 0
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US-08-978-217-2 (1-371) x US-10-025-380-944 (1-563)

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QY 74 AsptRplleSeRTYrGlnValAGluLyAsnLySTYrAspAlaSerAlaIleAspPheSer 93
Db 562 GACTGATCAGCTACCAAGTGAAGAACAAGTACGACGCAAGCCATTGACTTCTCA 503
QY 94 ArgCYsAspMetAspGlyAlaThrLeuCYsAsnCysAlaLeuGluGluLeuArgLeuVal 113
Db 502 CGATGATCAGTGAATGGCGCCACCTCTGCAATTGTGCTTGAGAGAGCTCGTGGTC 443
QY 114 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSer 133
Db 442 TTGGGCTCTGGGGGACCAACTCCATGCCAGCTGCAGACCTCCTCAGCTCTTCT 383
QY 134 AspGluLeuSerTrpIleIleGluLeuLeuGluLyAspGlyMetAlaPheGlnGluAla 153
Db 382 GATAGCTCAGTTGGATCATTGAAGCTGCTGAGAGAGATGGCATGGCTTCCAGAGAGCC 323
QY 154 LeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGly 173
Db 322 CTAGACCCAGGGCCCTTTGACCAAGGCGACCCCTTTGCCAGAGAGCTGCTGAGAGCGGT 263
QY 174 GlnGlnAlaSerProTyRHisProGlySerCysGlyAlaGlyAlaProSerProGlySer 193
Db 262 CAGCAAGCCAGCCCTTACACCCCGGCGAGCTGTGGCGCAGAGAGCCCTCCCGGCGAGC 203
QY 194 SerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGly 213
Db 202 TCTAGCTCTCCACCGAGGAGGAGTGGTCTTCTCGAGCTCCCATCTCCAGACTCCGGT 143
QY 214 GlySerAspValaAspLeuAspProThrAspGlyLyLeuPheProSerAspGlyPheArg 233
Db 142 GGAAGTACGTCGAGACCTGGATCCCATGATGCAAGCTCTTCCCGAGGATGGTTTGGT 83
QY 234 AspCysLySlySlyGlyAspProLyHisGlyLySargLySargLyAlaArgProArgLyLeu 253
Db 82 GACGCAAGAGAGGGGAGATCCCAAGCAGCGGAAACGAGGCGCGCCCGAAAGCTG 23
QY 254 SerLySlyLySlyGlyAspProLyHisGlyLySargLySargLyAlaArgProArgLyLeu 260
Db 22 AGCAAGAGTACTGGAGCTGT 2
RESULT 12
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US-09-922-217-944/C
Sequence 944, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugui
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922.217
NUMBER OF SEQ ID NOS: 2001-08-03
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 944
LENGTH: 563
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-944
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Alignment Scores:
Pred. No.: 2,41e-90 Length: 563
Score: 1011.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.06% Indels: 0
DB: Gaps: 0
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US-08-978-217-2 (1-371) x US-09-922-217-944 (1-563)

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QY 74 AsptRplleSeRTYrGlnValAGluLyAsnLySTYrAspAlaSerAlaIleAspPheSer 93
Db 562 GACTGATCAGCTACCAAGTGAAGAACAAGTACGACGCAAGCCATTGACTTCTCA 503
QY 94 ArgCYsAspMetAspGlyAlaThrLeuCYsAsnCysAlaLeuGluGluLeuArgLeuVal 113
Db 502 CGATGATCAGTGAATGGCGCCACCTCTGCAATTGTGCTTGAGAGAGCTCGTGGTC 443
QY 114 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSer 133
Db 442 TTGGGCTCTGGGGGACCAACTCCATGCCAGCTGCAGACCTCCTCAGCTCTTCT 383
QY 134 AspGluLeuSerTrpIleIleGluLeuLeuGluLyAspGlyMetAlaPheGlnGluAla 153
Db 382 GATAGCTCAGTTGGATCATTGAAGCTGCTGAGAGAGATGGCATGGCTTCCAGAGAGCC 323
QY 154 LeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGly 173
Db 322 CTAGACCCAGGGCCCTTTGACCAAGGCGACCCCTTTGCCAGAGAGCTGCTGAGAGCGGT 263
QY 174 GlnGlnAlaSerProTyRHisProGlySerCysGlyAlaGlyAlaProSerProGlySer 193
Db 262 CAGCAAGCCAGCCCTTACACCCCGGCGAGCTGTGGCGCAGAGAGCCCTCCCGGCGAGC 203
QY 194 SerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGly 213
Db 202 TCTAGCTCTCCACCGAGGAGGAGTGGTCTTCTCGAGCTCCCATCTCCAGACTCCGGT 143
QY 214 GlySerAspValaAspLeuAspProThrAspGlyLyLeuPheProSerAspGlyPheArg 233
Db 142 GGAAGTACGTCGAGACCTGGATCCCATGATGCAAGCTCTTCCCGAGGATGGTTTGGT 83
QY 234 AspCysLySlySlyGlyAspProLyHisGlyLySargLySargLyAlaArgProArgLyLeu 253
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Db 82 GACTGCAGAGAGGGGAGTCCACAGCAGGGAGGAGGAGCCCGCCGAGAAAGCTG 23
 Oy 254 SerlysglyttrtpaspCys 260
 |||||
 Db 22 AGCAAGAGTACTGGGACTGT 2

RESULT 13
 US-09-833-263-944/c
 ; Sequence 944, Application US/09833263
 ; Patent No. US20020110547A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Meagher, Madeleine J.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.471C12
 ; CURRENT APPLICATION NUMBER: US/09/833,263
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 1093
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 944
 ; LENGTH: 563
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-833-263-944

Alignment Scores:
 Pred. No.: 2,41e-90 Length: 563
 Score: 1011.00 Matches: 187
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 51.06% Indels: 0
 DB: 10 Gaps: 0

US-08-978-217-2 (1-371) x US-09-833-263-944 (1-563)

Oy 74 AAPTPLIESERTYGLINVALGLULYSAENLYTYRASPALASERLAIIEAPHPSESER 93
 |||||
 Db 562 GACTGATAGCTACCAATGAGAGAAACAACTACGAGCAAGCCCACTTGACTTCTCA 503
 Oy 94 AAGCYAASPMECTASPGIYLAATHREUCYBAANCYBAALILEUGLULYEAUARYLEUVAL 113
 |||||
 Db 502 CGATGAGATAGATGGCGCCACCTCTCAATTGTGCCCTTGAGAGAGCTGCGTCTGTC 443
 Oy 114 PHEGIYPRLEUGLYASPGILNLEUHSALAGINLEUARYASPEUARYSERSESER 133
 |||||
 Db 442 TTTGGCCCTCTGGGGGACCACTCCATGCCAGCTGCGAGACCTCACTTCCAGCTTCT 383
 Oy 134 AEPGLULESERTRPILEIEGLEULEUGLULYASPGIYMERALAPHEGINLUALA 153
 |||||
 Db 382 GATGAGCTAGTTGATCATTTGAGCTGCTGGAGAAAGATGGCATGGCTTCCAGAGGCC 323
 Oy 154 LEUASPPROGIYPROPHASPGINGIYSERPROPHALIGINGIULEUASPAAPGIY 173
 |||||
 Db 322 CTAGACCCAGGGCCCTTTGACCAAGGAGCCCTTTGCCAGGAGCTGTGCGACGAGCT 263
 Oy 174 GINGINLASERPROTYRHSIPROGIYSEYSGIYALIGIYALAPROSERPROGIYSER 193
 |||||
 Db 262 CAGCAAGCCAGCCCTTACCAACCCCGGACCTGTGGCGAGAGCCCTTCCCGCCGAGCC 203
 Oy 194 SERRASPVASERTHRLAGLYTHRGYALASERASERSETHIASERASERASERGIY 213
 |||||
 Db 202 TGTGACGTCTCCACCCAGAGAGTGTGCTTCTCGAGCTCCCACTCTCCAGACTCCGCT 143
 Oy 214 GYSEASPVASVALASPEUASPPROTHASPGIYLYSLEUPHEBROSERASPGIYPHEARG 233
 |||||
 Db 142 GGAAGTACGTGAGCTGTGATCCCACTGATGGCAAGCTCTTCCCGAGCATGTTTTCGT 83
 Oy 234 AAPCYBLVLYSGIYASPPOLYSHISGLIYLYBATLYVAIRGLIYARPROARGLYLSLEU 253
 |||||
 Db 82 GACTGCAGAGAGGGGAGTCCACAGCAGGGAGGAGGAGGAGCCCGCCGAGAAAGCTG 23

Oy 254 SerlysglyttrtpaspCys 260
 |||||
 Db 22 AGCAAGAGTACTGGGACTGT 2

RESULT 14
 US-10-076-622-282
 ; Sequence 282, Application US/10076622
 ; Publication No. US20030023036A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Persing, David H.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C11
 ; CURRENT APPLICATION NUMBER: US/10/076,622
 ; CURRENT FILING DATE: 2002-02-13
 ; NUMBER OF SEQ ID NOS: 627
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 282
 ; LENGTH: 502
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-076-622-282

Alignment Scores:
 Pred. No.: 7.55e-80 Length: 502
 Score: 903.00 Matches: 166
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 45.61% Indels: 0
 DB: 9 Gaps: 0

US-08-978-217-2 (1-371) x US-10-076-622-282 (1-502)

Oy 184 CYSGIYALAGIYALAPROSERPROGIYSESERASPVASERTHRLAGLYTHRGIYLA 203
 |||||
 Db 3 TGTGCGAGAGAGGCCCTCCCGGAGCTTGACGTCTCCACCGAGGAGCTGGTCT 62
 Oy 204 SERASERSETHIASERASERASERGIYGLYSEASPVASLEUASPPROTHAS 223
 |||||
 Db 63 TTTGAGCTCTCCCACTCTCTCAACTCCGCTGGAAGTACCTGAGCTTCCCACTGAT 122
 Oy 224 GYLYSLEUPHEPROSERASPGIYPHEARGASPCYSLYSGIYASPPOLYSHISGLIY 243
 |||||
 Db 123 GGCAGCTCTTCCCAAGGAGTGTGTTTCTGTGACTCAAGAGGGGATCCCAAGCAGGG 182
 Oy 244 LYBATGLYBATGLYAIRPROARGLYLSLEUSERLYSGIYLYTTPASPCYBLEUGLULY 263
 |||||
 Db 183 AAGCCGAAACGAGGCCGCGCCCGAAGCTGAGCAAGAGTACTGGAGCTGTCTGAGGGCC 242
 Oy 264 LYSLSERLYSHISALAPROARGLYTHRLISLEUTRPGIUPHEILARASPILEU 283
 |||||
 Db 243 AAGAGAGCAGCAGCGCCCGCAGAGGACCCACCTGTGGAGTTATCCGGACATCTCTC 302
 Oy 284 ILEHISPROGIULEUASNGIULYLEUWELYSTIPGLIASNARGHISGLIYLYALPHE 303
 |||||
 Db 303 ATCCACCCGAGACTCAAGAGGGCTCATGAAGTGGAGAAATCGGCATGAGAGCGCTTTC 362
 Oy 304 LYSPELEUASERSEGLUALVALALAGINLEUTRPGIYGLINLYLYLYASNSERSEN 323
 |||||
 Db 363 AAGTCTCTGCGCTCCGAGAGCTGTGCCCCCAACTATGGGGCCAAAGAAAGAACGAGAAC 422
 Oy 324 METTRTYRGLULYLSLEUSERARGHAMELRARGTYRTRYRFLYVARGGLULILEUGLU 343
 |||||
 Db 423 ATGACCTTCGAGAACTGAGCCGGGCAATGAGTACTACTACAAAGGAGATCTTGAAA 482
 Oy 344 ARGVALASPGIYARGARG 349
 |||||
 Db 483 CGGTGATGGCCGGCGA 500

RESULT 15

